

OIEP

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/891,064A

DATE: 12/26/2001
 TIME: 11:39:22

Input Set : A:\754cip.seq.txt
 Output Set: N:\CRF3\12262001\I891064A.raw

ENTERED

5 <110> APPLICANT: James M. Anderson
 6 Christina M. Van Itallie
 8 <120> TITLE OF INVENTION: Human Occludin, Its Uses and Enhancement of Drug
 9 Absorption Using Occludin Inhibitors
 11 <130> FILE REFERENCE: OCR-754.CIP
 13 <140> CURRENT APPLICATION NUMBER: US 09/891,064A
 14 <141> CURRENT FILING DATE: 2001-06-25
 16 <150> PRIOR APPLICATION NUMBER: US 09/142,732
 17 <151> PRIOR FILING DATE: 1998-09-15
 19 <160> NUMBER OF SEQ ID NOS: 6
 20 <170> SOFTWARE: MS DOS
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 26 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 32 <221> NAME/KEY: mat_peptide
 34 <222> LOCATION: complete sequence
 36 <223> OTHER INFORMATION: human occludin
 38 <400> SEQUENCE: 1
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 42 agcccgcgcc tctcctctgc gcccgcctc tcgggcccga acatcgcgcg 150
 43 gttcctttaa cagcgcgctg gcagggtgtg ggaagcagga ccgcgtcctc 200
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 58 tctttgttac cagtgttata agatctgaaa tgtccagaac aagaagatac 950
 59 tacttaagtg tgataatagt gagtgtctatc ctgggcatca tgggtgtttat 1000
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 65 gacaggtatg acaagtccaa tattttgtgg gacaaggaa acatttatga 1300
 66 tgagcagccc cccaatgtcg aggagtgggt taaaaatgtg tctgcaggca 1350

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67 cacaggacgt gccttcaccc ccattctgact atgtggaaaag agttgacagt 1400
68 cccatggcat actcttccaa tggcaaagt aatgacaagc ggttttatcc 1450
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70 cattaacttc gcctgtggat gacttcaggc agcctcgtta cagcagcggg 1550
71 ggtaactttg agacaccttc aaaaagagca cctgcaaagg gaagagcagg 1600
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74 cctatcactt cagatcaaca aagacaactg tacaagagga attttgacac 1750
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76 aagaactctc ccgtttggat aaagaattgg atgactatag agaagaaagt 1850
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78 gggatctgca gattacaaaa gtaagaagaa tcattgcaag cagttaaaga 1950
79 gcaaattgtc acacatcaag aagatggttg gagactatga tagacagaaa 2000
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81 ctgcaatctt ctgagaaggc aaatgacttt ggaccataac cccggaagcc 2100
82 aaacctctgt gagcatcaca aagttttggg ttgctttaac atcatcagta 2150
83 ttgaagcatt ttataaatcg cttttgataa tcaactgggc tgaacaactc 2200
84 caattaagga ttttatgctt taaacattgg ttcttgtatt aagaatgaaa 2250
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86 ctttcacacc cc 2312
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97 <220> FEATURE:
99 <221> NAME/KEY: peptide
101 <222> LOCATION: complete sequence
103 <223> OTHER INFORMATION: human occludin
105 <400> SEQUENCE: 2
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111 20 25 30
113 Gly Glu Met His Val Arg Pro Met Leu Ser Gln Pro Ala Tyr Ser
114 35 40 45
116 Phe Tyr Pro Glu Asp Glu Ile Leu His Phe Tyr Lys Trp Thr Ser
117 50 55 60
119 Pro Pro Gly Val Ile Arg Ile Leu Ser Met Leu Ile Ile Val Met
120 65 70 75
122 Cys Ile Ala Ile Phe Ala Cys Val Ala Ser Thr Leu Ala Trp Asp
123 80 85 90
125 Arg Gly Tyr Gly Thr Ser Leu Leu Gly Gly Ser Val Gly Tyr Pro
126 95 100 105
128 Tyr Gly Gly Ser Gly Phe Gly Ser Tyr Gly Ser Gly Tyr Gly Tyr
129 110 115 120
131 Gly Tyr Gly Tyr Gly Tyr Gly Tyr Gly Tyr Thr Asp Pro Arg
132 125 130 135
134 Ala Ala Lys Gly Phe Met Leu Ala Met Ala Ala Phe Cys Phe Ile
135 140 145 150

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137	Ala	Ala	Leu	Val	Ile	Phe	Val	Thr	Ser	Val	Ile	Arg	Ser	Glu	Met
138					155					160					165
140	Ser	Arg	Thr	Arg	Arg	Tyr	Tyr	Leu	Ser	Val	Ile	Ile	Val	Ser	Ala
141					170					175					180
143	Ile	Leu	Gly	Ile	Met	Val	Phe	Ile	Ala	Thr	Ile	Val	Tyr	Ile	Met
144					185					190					195
146	Gly	Val	Asn	Pro	Thr	Ala	Gln	Ser	Ser	Gly	Ser	Leu	Tyr	Gly	Ser
147					200					205					210
149	Gln	Ile	Tyr	Ala	Leu	Cys	Asn	Gln	Phe	Tyr	Thr	Pro	Ala	Ala	Thr
150					215					220					225
152	Gly	Leu	Tyr	Val	Asp	Gln	Tyr	Leu	Tyr	His	Tyr	Cys	Val	Val	Asp
153					230					235					240
155	Pro	Gln	Glu	Ala	Ile	Ala	Ile	Val	Leu	Gly	Phe	Met	Ile	Ile	Val
156					245					250					255
158	Ala	Phe	Ala	Leu	Ile	Ile	Phe	Phe	Ala	Val	Lys	Thr	Arg	Arg	Lys
159					260					265					270
161	Met	Asp	Arg	Tyr	Asp	Lys	Ser	Asn	Ile	Leu	Trp	Asp	Lys	Glu	His
162					275					280					285
164	Ile	Tyr	Asp	Glu	Gln	Pro	Pro	Asn	Val	Glu	Glu	Trp	Val	Lys	Asn
165					290					295					300
167	Val	Ser	Ala	Gly	Thr	Gln	Asp	Val	Pro	Ser	Pro	Pro	Ser	Asp	Tyr
168					305					310					315
170	Val	Glu	Arg	Val	Asp	Ser	Pro	Met	Ala	Tyr	Ser	Ser	Asn	Gly	Lys
171					320					325					330
173	Val	Asn	Asp	Lys	Arg	Phe	Tyr	Pro	Glu	Ser	Ser	Tyr	Lys	Ser	Thr
174					335					340					345
176	Pro	Val	Pro	Glu	Val	Val	Gln	Glu	Leu	Pro	Leu	Thr	Ser	Pro	Val
177					350					355					360
179	Asp	Asp	Phe	Arg	Gln	Pro	Arg	Tyr	Ser	Ser	Gly	Gly	Asn	Phe	Glu
180					365					370					375
182	Thr	Pro	Ser	Lys	Arg	Ala	Pro	Ala	Lys	Gly	Arg	Ala	Gly	Arg	Ser
183					380					385					390
185	Lys	Arg	Thr	Glu	Gln	Asp	His	Tyr	Glu	Thr	Asp	Tyr	Thr	Thr	Gly
186					395					400					405
188	Gly	Glu	Ser	Cys	Asp	Glu	Leu	Glu	Glu	Asp	Trp	Ile	Arg	Glu	Tyr
189					410					415					420
191	Pro	Pro	Ile	Thr	Ser	Asp	Gln	Gln	Arg	Gln	Leu	Tyr	Lys	Arg	Asn
192					425					430					435
194	Phe	Asp	Thr	Gly	Leu	Gln	Glu	Tyr	Lys	Ser	Leu	Gln	Ser	Glu	Leu
195					440					445					450
197	Asp	Glu	Ile	Asn	Lys	Glu	Leu	Ser	Arg	Leu	Asp	Lys	Glu	Leu	Asp
198					455					460					465
200	Asp	Tyr	Arg	Glu	Glu	Ser	Glu	Glu	Tyr	Met	Ala	Ala	Ala	Asp	Glu
201					470					475					480
203	Tyr	Asn	Arg	Leu	Lys	Gln	Val	Lys	Gly	Ser	Ala	Asp	Tyr	Lys	Ser
204					485					490					495
206	Lys	Lys	Asn	His	Cys	Lys	Gln	Leu	Lys	Ser	Lys	Leu	Ser	His	Ile
207					500					505					510
209	Lys	Lys	Met	Val	Gly	Asp	Tyr	Asp	Arg	Gln	Lys	Thr			

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234                               20
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240 <211> LENGTH: 24
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244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
248 <221> NAME/KEY: peptide
250 <223> OTHER INFORMATION: construct used in experiments
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272 <221> NAME/KEY: peptide
274 <223> OTHER INFORMATION: construct used in experiments
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290 <212> TYPE: PRT
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
296 <221> NAME/KEY: peptide
298 <223> OTHER INFORMATION: construct used in experiments
300 <400> SEQUENCE: 6
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VERIFICATION SUMMARY

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